Amendments to the Specification:

On page 4, please amend the paragraph starting on line 46 as follows:

-- FIG. 8 shows a map of locations for various DNA sequence motifs within the cLysMAR. FIG. 8 (B) represents a Map of locations for various DNA sequence motifs within the cLysMAR. Vertical lines represent the position of the computer-predicted sites or sequence motifs along the 3034 base pairs of the cLysMAR and its active regions, as presented in FIG. 5. The putative transcription factor sites, (MEF2 05, Oct-1, USF-02, GATA, NFAT) for activators and (CDP, SATB1, CTCF, ARBP/MeCP2) for repressors of transcription, were identified using MatInspector (Genomatix), and CpG islands were identifed with CPGPLOT. Motifs previously associated with MAR elements are labelled in black and include CpG dinucleotides and CpG islands, unwinding motifs (AATATATT and MTATT), poly As and Ts, poly Gs and Cs, Drosophila topoisomerase II binding sites (GTNWAYATTNATTNATNNR (SEQ ID NO: 242)) which had identity to the 6 bp core and High mobility group I (HMG-I/Y) protein binding sites. Other structural motifs include nucleosome-binding and nucleosome disfavouring sites and a motif thought to relieve the superhelical strand of DNA. FIG. 8(A) represents the comparison of the ability of portions of the cLysMAR to activate transcription with MAR prediction score profiles with MarFinder. The top diagram shows the MAR fragment activity as in FIG. 5, while the middle and bottom curves show MARFinder-predicted potential for MAR activity and for bent DNA structures respectively. – -

On page 9, please amend the paragraph starting on line 19 as follows:

-- "MARs", according to a well-accepted model, may mediate the anchorage of specific DNA sequence to the nuclear matrix, generating chromatin loop domains that extend outwards from the heterochromatin cores. While MARs do not contain any obvious consensus or recognizable sequence, their most consistent feature appears to be an overall high A/T content, and C bases predominating on one strand (Bode J, Schlake T, RiosRamirez M, Mielke C, Stengart M, Kay V and KlehrWirth D, "Scaffold/matrix-attached regions: structural propreties creating transcriptionally active loci", Structural and Functional Organization of the Nuclear Matrix: International Review of Citology, 162A:389453, 1995). These regions have a propensity to form

bent secondary structures that may be prone to strand separation. They are often referred to as base-unpairing regions (BURs), and they contain a core-unwinding element (CUE) that might represent the nucleation point of strand separation (Benham C and al., Stress induced duplex DNA destabilization in scaffold/matrix attachment regions, J. MoL BioL, 274:181-196, 1997). Several simple AT-rich sequence motifs have often been found within MAR sequences, but for the most part, their functional importance and potential mode of action remain unclear. These include the A-box (AATAAAYAAA (SEQ ID NO: 243)), the T-box (TTWTWTTWTT(SEQ ID NO: 244)), DNA unwinding motifs (AATATATT, AATATT), SATB1 binding sites (H-box, A/T/C25) and consensus Topoisomerase II sites for vertebrates (RNYNNCNNGYNGKTNYNY(SEQ ID NO: 245)) or Drosophila (GTNWAYATTNATNNR (SEQ ID NO: 246)). --